Supplementary Table 1. Number of samples, genotyping platforms in this study.

Ethnic groups	Stage 1				Stage 2			Further validation		
	Subjects (KD/Conrol)	Platform	No of autosomal SNVs		Subjects (KD/Conrol)	Platform	No of SNVs analyzed	Subjects (KD/Conrol)	Platform	No of SNVs analyzed
			Genotyped	Genotyped or imputed[a]						
Japan	428/3379	Illumina Human Hap550/610	433854	7817912	1418/1700	Invader	48	1758/653	Invader	2
Taiwan	662/1107	Affymetrix SNP 6.0	697571	7391440	261/567	Sequenom MassARRAY or TaqMan	48	-	-	-
Korea	186/600	Affymetrix SNP 6.0	607758	7134078	473/484	VeraCode GoldenGate or TaqMan	48	-	-	-

KD, Kawasaki disease; SNV, single nucleotide variant

[a] QC'd: MAF≥0.01 & info≥0.4

Supplementary Table 2. Sequences of the PCR primers and probes for Invader assay to genotype SNVs in *IGHV* gene region.

Genes	**PCR primers**		**SNVs**	**Alleles[a] 1/2**	**Probes for Invader assay[b]**	
IGHV3-43	Forward	GATCAGCACTGAACACAGAGAAYG	rs61999676	A/C	Allele1	TGGGATGGTGGTAGCAC
	Reverse	TGCAGATACAGGGAGTTTTTGCTGTT			Allele2	GGGGATGGTGGTAGCA
					Invader	GAAGGGTCTGGAGTGGGTCTCTCTTATTAGTA
			rs79008247	A/C	Allele1	ACTCCCCCAGACTCC
					Allele2	CCTCCCCCAGACTC
					Invader	TCTCAGGGACCCCCCAGGCTGTACCACGT
IGHV1-45	Forward	RTARTTGGTGTTACCATTGAAAGGTG	rs7141669	C/T	Allele1	GGACAAGCGCTTGAGT
	Reverse	AGTCCAGTCAAGGTGGCTTTT			Allele2	AGACAAGCGCTTGAGTG
					Invader	CACTGGGTGCGACAGGCCCCCT
IGHV3-48	Forward	CYGTGCTCAGTGTSCTGT	rs7148607	T/C	Allele1	AGTAGTACCATATACTACGC
	Reverse	GTGGCAGTTTCTGACCTTGG			Allele2	GGTAGTACCATATACTACG
					Invader	GGGCTGGAGTGGGTTTCATACATTAGTAGTAGTT
IGHV3-49	Forward	GTATTCTGHTGTCYCACCATMAGC	rs2073674	A/C	Allele1	TTCCGCCAGGCTCCA
	Reverse	GACCACCAACCATGGAGTTTG			Allele2	GTCCGCCAGGCTCC
					Invader	GGATTCACCTTTGGTGATTATGCTATGAGCTGGA
			rs2073673	G/T	Allele1	GTACCAAGCCTCCCC
					Allele2	TTACCAAGCCTCCCCC
					Invader	TAGCCAGGGCGGTCCCTGAGACTCT
IGHV1-58	Forward	CACTCAAGGCGTTGTCCAC	rs2516904	T/C	Allele1	TAGCAGAGCTAGTAAAGG
	Reverse	GGCTTTCATCCACTCCTGTG			Allele2	CAGCAGAGCTAGTAAAG
					Invader	ACGAGCCTGTCGCACCCACYGCAA
IGHV3-62	Forward	CCAGTATACAGTGTCCCAGGC	rs72483334	T/C	Allele1	ATACCGTACTCTACACAG
	Reverse	GTGTTTCCATTCSGTGATCAGC			Allele2	GTACCGTACTCTACACA
					Invader	GGTTTGKAGTGGGTCTCAGTTATTAGTACAAGTGGTGT
			rs113692972	A/T	Allele1	ATAGCAGAGCTACTGAAG
					Allele2	TTAGCAGAGCTACTGAAG
					Invader	TTTCYTRGAGCCTGGYGGACCCAGTGCC
IGHV3-64	Forward	AGGTTTCTGCATGGTCCCACAT	rs2072045	C/T	Allele1	GACTCHGTGAAGGGCAG
	Reverse	GGTGTTTTCATTTGGTGATCAGC			Allele2	AACTCHGTGAAGGGCAGATT
					Invader	GGAATATGTTTCAGCTAYYAGTARTAATGGGGGTAGCACATAYTAYGCAT
			rs11846079	T/C	Allele1	AAGGCTTGGTCCAGCC
					Allele2	GAGGCTTGGTCCAGC
					Invader	AGGTGCAGCTGGTGGAGTCTGGGGT
			rs2073670	A/G	Allele1	ATCATGACTCTTCTGTGTTC
					Allele2	GTCATGACTCTTCTGTGTT
					Invader	CAAGGAAAACCCMGCTCAGCCCAAASTCCT
IGHV3-66	Forward	ATGTGCATTTGGTGCATGAGAGGTT	rs6423677	A/C	Allele1	AGCTATAAATAACTGAGACCC
	Reverse	TGGATATGTGTGGCAGTTTCTAACCAA			Allele2	CGCTATAAATAACTGAGACC
					Invader	CACGGAGTCTGCGTAGTATGYGCTACCACT
			rs149638514	T/C	Allele1	ATCCAGCCTGGGGG
					Allele2	GTCCAGCCTGGGGG
					Invader	CAGCTGGTGGAGTCTGGRGGAGGCTTGT
intergenic	Forward	ACAATRGACAAAATGCAGATCTACAGA	rs4774175	G/A	Allele1	CGACAAAATGATCTCAAGAT
	Reverse	TCTTCCCTCAAACACAAATGTCCC			Allele2	TGACAAAATGATCTCAAGATAAT
					Invader	CCTGACACAAGCACATATGTCCAATGTTAAACTGTCTTGA
IGHV1-69	Forward	GGAAGGGATCCTGGTTTAGTTAAAGAG	rs8009570	G/A	Allele1	CAGCAAACTACGCACA
	Reverse	CTCAGCTCCATGTAGGCTGTG			Allele2	TAGCAAACTACGCACAG
					Invader	GCTTGAGTGGATGGGRGGGATCATCCCTATCYTTGGTAA
			rs55891010	A/G	Allele1	AGATAGGGATGATCCY
					Allele2	GGATAGGGATGATCC
					Invader	TCTGCCCTGGAACTTCTGTGCGTAGTTTGCTRTACCAAT
			rs11845244	C/T	Allele1	CTCCCATCCACTCAAG
					Allele2	TTCCCATCCACTCAAGC
					Invader	GTGCGTAGTTTGCTRTACCAARGATAGGGATGATCCA
IGHV2-70	Forward	GTACTTCAGAAGCAAAAAATCTATTCTCTCC	rs2073669	A/C	Allele1	AGTGCAAGCCACTCCAG
	Reverse	CTCTGTGGTATCCGTGCACAG			Allele2	CGTGCAAGCCACTCCA
					Invader	CTTCAGAGATGTGCTGYAGWATTTATCATCATCCCAATCAATGT

PCR, polymerase chain reaction; SNVs, single-nucleotide variants.

[a] Risk-associated alleles are underlined.

[b] Nucleotides corresponding to variant positions are shown in red characters.

Supplementary Table 3. Sequences of the primers for PCR and direct sequencing of rs6423677.

PCR Forward	ATGTGCATTTGGTGCATGAGAGGTT
PCR Reverse	TGGATATGTGTGGCAGTTTCTAACCAA
Sequencing	GTAATACACAGCCGTGTCCTCA

PCR, polymerase chain reaction

Supplementary Table 4. Primers and their sequences used in the immunoglobulin heavy chain repertoire library preparation.

Primers	Sequence	Length
1st PCR		
Forward primers[a]		
VH1-FR1-tailed	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTGGCCTCAGTGAAGGTCTCCTGCAAG	59
VH2-FR1-tailed	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTGTCTGGTCCTACGCTGGTGAAACCC	59
VH3-FR1-tailed	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTCTGGGGGGTCCCTGAGACTCTCCTG	59
VH4-FR1-tailed	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTCTTCGGAGACCCTGTCCCTCACCTG	59
VH5-FR1-tailed	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTCGGGGAGTCTCTGAAGATCTCCTGT	59
VH6-FR1-tailed	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTTCGCAGACCCTCTCACTCACCTGTG	59
Reverse primers[b]		
IgM-tailed	TCTTTCCCTACACGACGCTCTTCCGATCTNNNNAGGCTATAGGGAAGGAAGTCCTGTGCGAG	62
IgD-tailed	TCTTTCCCTACACGACGCTCTTCCGATCTNNNNTCAGAGCCGGGAACACATCCGGAGCCTTG	62
IgG-tailed	TCTTTCCCTACACGACGCTCTTCCGATCTNNNNGCCTCTATGACCAGGCAGCCCAGGGC	59
IgA-tailed	TCTTTCCCTACACGACGCTCTTCCGATCTNNNNAGGATAGGGAAGAAGCCCTGGACCAGGCA	62
2nd PCR[c]		
P7-2nd-PCR_idx (Fwd)	CAAGCAGAAGACGGCATACGAGATXXXXXXGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT	64
P5-2nd-PCR (Rev)	AATGATACGGCGACCACCGAGATCTACACTCTTTCCCTACACGACGCTCTTCCGATCT	58

[a] Sequence tag for annealing with the 2nd forward primer is highlighted in red. Primers were created in the framework region 1 sequence which is shared within each *IGHV* gene group. VH1-FR1-tailed covers both *IGHV1* and *IGHV7* genes.

[b] Sequence tag for annealing with the 2nd reverse primer is highlighted in red. Primers were designed in the constant region sequence specific to each immunoglobulin class. Twelve nucleotides including random tetramer for distinguishing adjacent clusters are written in blue letters.

[c] Sequence tags for binding of the amplicons to the flow cell are highlighted in red. The forward primer has a 6-mer barcode sequence for identifying the samples (blue letters).

Supplementary Table 5. Loci with association signals of $P < 5.0 \times 10^{-8}$ in the meta-analysis of three GWAS results.

SNV groups	Chromosome	Region[a]	Genes within the region	Most significant SNVs in the region			
				dbSNP ID	**P value**	**Nearest gene**	**Position in genes**
1	4	185481949-185699898	*CASP3, CCDC111, MLF1IP, IRF2, ACSL1*	rs2720377	2.66×10^{-9}	*CASP3*	intron
2	6	30940387-32834732	*LTA, NFKBIL1, HLA-DRA, MICB, MCCD1*	rs2844485	3.66×10^{-8}	*LTA*	intron
3	6	31436581-32818678	*HLA-DRB5, HLA-DRB1, BTNL2, HLA-DQA1, NFKBIL1*	rs73729123	$9.72 \times 10\text{-}^{10}$	*HLA-DRB5*	5' flanking
4	6	32198847-32788987	*C6orf10, HLA-DRA, BTNL2, HLA-DRB1, HLA-DQA1*	rs7739458	4.57×10^{-11}	*LOC101929163*	intron
5	6	32365707-32711984	*HLA-DQB1, BTNL2, HLA-DQA2, HLA-DQA1*	rs146650659	5.62×10^{-9}	*HLA-DQB1*	5' flanking
6	8	11287081-11402063	*BLK, FAM167A, C8orf12*	rs2736340	1.23×10^{-16}	*BLK*	5' flanking
7	16	85957793-85981482	*IRF8*	rs13330932	4.07×10^{-8}	*LOC107984811*	5' flanking
8	19	41147617-41369634	*ITPKC, C19orf54, ADCK4, RAB4B, MIA*	rs28493229	3.07×10^{-9}	*ITPKC*	intron
9	20	44629290-44779794	*CD40, NCOA5, SLC12A5, MMP9*	rs1883832	1.76×10^{-8}	*CD40*	5' untranslated region

[a] Chromosomal regions surrounding the top significant SNVs and SNVs in 1000 Genomes with r^2>0.1 in the EAS population.

SNV locations are based on NCBI human genome reference Build 37.3.

GWAS, genome-wide association study; SNV, single nucleotide variant

Supplementary Table 6. SNVs expected to achieve *P* values smaller than 5.0 × 10^{-8} at probability higher than 0.8.

				SNVs with highest probability				SNVs with lowest P value in GWAS meta-analysis			
Chr	Region[a,b]	N of SNVs with probability > 0.8	N of SNVs with probability > 0.5	dbSNP ID	Position[b]	*P* values in GWAS meta-analysis	Simulation score	dbSNP ID	Position[b]	*P* values in GWAS meta-analysis	Simulation score
1	77550431-77740836	4	48	rs4546965	77641160	1.82×10^{-6}	0.96	rs78640576	77650483	1.45×10^{-6}	0.93
2	56096573-56600739	4	4	rs56120846	56152091	1.12×10^{-5}	0.84	rs72811720	56147089	1.03 × 10-5	0.82
2	56150402-56260481	1	2	rs752816	56258606	6.04×10^{-6}	0.81	rs752816	56258606	6.04 × 10-6	0.81
2	130252857-130424555	1	47	rs66974421	130401804	2.28×10^{-5}	0.81	rs66974421	130401804	2.28 × 10-5	0.81
2	174293213-174307764	3	4	rs16861684	174306514	4.95×10^{-5}	0.82	rs16861684	174306514	4.95 × 10-5	0.82
2	207723592-207838388	9	15	rs75295922	207814273	1.20×10^{-7}	0.97	rs75295922	207814273	1.20 × 10-7	0.97
3	36487492-36537816	3	21	rs936154	36487492	3.15×10^{-5}	0.83	rs936154	36487492	3.15 × 10-5	0.83
3	143754128-143967771	1	1	rs181511609	143957304	5.86×10^{-7}	0.83	rs181511609	143957304	5.86 × 10-7	0.83
4	109311641-109371870	1	23	rs219474	109313182	2.06×10^{-5}	0.82	rs219474	109313182	2.06 × 10-5	0.82
4	166615296-166661136	5	16	rs2611259	166619952	2.04×10^{-6}	0.91	rs2611259	166619952	2.04 × 10-6	0.91
4	185481949-185699898	103	121	rs2720377	185564746	2.66×10^{-9}	1.00	rs2720377	185564746	2.66 × 10-9	1.00
4	185817577-185873031	4	31	rs6552852	185857061	1.59×10^{-5}	0.91	rs6552852	185857061	1.59 × 10-5	0.91
5	36786459-37583716	69	157	rs292160	36896073	1.95×10^{-5}	0.92	rs2133786	36796752	1.03 × 10-5	0.86
5	61352528-61691357	1	27	rs10060036	61366182	5.15×10^{-5}	0.81	rs10060036	61366182	5.15 × 10-5	0.81
5	126089582-126181193	1	12	rs62391744	126165480	1.60×10^{-5}	0.82	rs62391744	126165480	1.60 × 10-5	0.82
6	25415117-26557121	3	79	rs407934	25504562	9.04×10^{-8}	0.98	rs407934	25504562	9.04 × 10-8	0.98
6	25462110-32709346	26	161	rs1778477	28248594	9.57×10^{-6}	0.89	rs55645051	28168945	6.44 × 10-6	0.84
6	26678512-28984755	213	313	rs1873212	27869631	3.90×10^{-7}	0.97	rs1873212	27869631	3.90 × 10-7	0.97
6	27297830-31678028	58	1008	rs1264516	30411903	1.83×10^{-6}	0.96	rs1264516	30411903	1.83 × 10-6	0.96
6	29036444-32881527	2	22	rs4504509	32399159	1.87×10^{-7}	0.99	rs4504509	32399159	1.87 × 10-7	0.99
6	29654409-30063301	1	117	rs1632885	29912510	2.55×10^{-5}	0.80	rs1632885	29912510	2.55 × 10-5	0.80
6	30940387-32834732	28	106	rs2857602	31533378	5.85×10^{-8}	1.00	rs2844485	31534206	3.66 × 10-8	0.99
6	31436581-32818678	221	574	rs9270560	32560741	6.80×10^{-9}	0.83	rs73729123	32519811	9.72×10^{-10}	0.99
6	32120391-32336495	1	3	rs3129960	32300809	1.77×10^{-6}	0.89	rs3129960	32300809	1.77 × 10-6	0.89
6	32198847-32788987	599	724	rs189914842	32353900	4.57×10^{-11}	1.00	rs189914842	32353900	4.57×10^{-11}	1.00
6	32365707-32711984	16	99	rs146650659	32646807	5.62×10^{-9}	1.00	rs146650659	32646807	5.62 × 10-9	1.00
6	32626537-32804934	13	81	rs2071473	32782605	6.71×10^{-6}	0.96	rs2071473	32782605	6.71 × 10-6	0.96
6	156667058-156697525	1	26	rs9480311	156667058	2.38×10^{-5}	0.80	rs9480311	156667058	2.38 × 10-5	0.80
7	52728131-52786995	3	10	rs75400473	52779924	1.23×10^{-5}	0.88	rs75400473	52779924	1.23 × 10-5	0.88
7	52796874-52945477	153	415	rs1919542	52862859	1.42×10^{-5}	0.90	rs77282866	52823787	3.32 × 10-6	0.88
7	106261427-106302691	1	3	rs146912378	106271117	4.48×10^{-6}	0.80	rs146912378	106271117	4.48 × 10-6	0.80
7	134057403-134154848	1	6	rs1791001	134125056	5.61×10^{-5}	0.84	rs1791001	134125056	5.61 × 10-5	0.84
8	11287081-11402063	117	121	rs2736340	11343973	1.23×10^{-16}	1.00	rs2736340	11343973	1.23×10^{-16}	1.00
10	27961690-28251697	48	65	rs12217663	27998085	7.53×10^{-6}	0.92	rs12217663	27998085	7.53 × 10-6	0.92
10	117945652-117955687	3	3	rs2251348	117952736	2.04×10^{-6}	0.88	rs2251348	117952736	2.04 × 10-6	0.88
11	11400471-11405591	1	7	rs113420414	11405402	9.20×10^{-6}	0.80	rs113420414	11405402	9.20 × 10-6	0.80
12	97876172-97979866	3	35	rs7309372	97894261	3.51×10^{-5}	0.85	rs7963257	97916472	1.27 × 10-5	0.84

13	29050843-29110535	1	16	rs12428318	29096824	1.47×10^{-5}	0.84	rs12428318	29096824	1.47 × 10-5	0.84
14	35896228-36190207	4	10	rs36099421	35978493	4.56×10^{-6}	0.88	rs36099421	35978493	4.56 × 10-6	0.88
14	52334589-52368588	2	16	rs10145910	52334931	2.64×10^{-5}	0.84	rs79706126	52340677	2.48 × 10-5	0.81
14	106876257-107254267	86	519	rs4774175	107152027	2.97×10^{-5}	0.88	rs61999181	106909420	1.69 × 10-6	0.82
15	70468924-70548169	1	6	rs11631322	70479558	1.14×10^{-5}	0.84	rs11631322	70479558	1.14 × 10-5	0.84
16	85957793-85981482	2	20	rs13330932	85974507	4.07×10^{-8}	0.98	rs13330932	85974507	4.07 × 10-8	0.98
17	49481612-49539720	3	14	rs62062092	49502284	7.77×10^{-6}	0.85	rs55809698	49504291	7.49 × 10-6	0.84
18	32778939-32980210	3	31	rs4799377	32844749	3.34×10^{-5}	0.82	rs4799377	32844749	3.34 × 10-5	0.82
19	17234471-17263091	4	13	rs12979647	17242941	3.18×10^{-5}	0.83	rs11670224	17238170	2.94 × 10-5	0.82
19	41147617-41369634	50	64	rs28493229	41224204	3.07×10^{-9}	1.00	rs28493229	41224204	3.07 × 10-9	1.00
20	16377100-16403927	1	2	rs6111093	16382725	2.38×10^{-5}	0.82	rs6111093	16382725	2.38 × 10-5	0.82
20	44629290-44779794	58	68	rs6032662	44734310	2.04×10^{-8}	1.00	rs1883832	44746982	1.76 × 10-8	0.98

[a] Chromosomal regions surrounding the top significant SNVs and SNVs in 1000 Genomes with r^2>0.1 in the EAS population.

[b] Location of the SNVs are based on NCBI human genome reference Build 37.3.

GWAS, genome-wide association study; SNV, single nucleotide variant

Supplementary Table 7. Association data of top 48 loci in the GWAS and the follow up studies in Japan, Korea and Taiwan and the results of meta-analyses.

Chromosome	dbSNP ID	Location[a]	Alleles		GWAS						Follow-up						Combined meta-analysis[b]			Closest genes	Position within genes
			Ref	Alt	Japan KD 428 Control 3079		Korea KD 186 Control 600		Taiwan KD 622 Control 1107		Japan KD 1418 Control 1700		Korea KD 473 Control 484		Taiwan KD 261 Control 567		*P*	OR [95% CI]	*QE P*		
					OR	*P*	OR	*P*	OR	*P*	OR	*P*	OR	*P*	OR	*P*					
1	rs78640576	77650483	C	T	0.74	2.93×10^{-3}	0.68	8.29×10^{-3}	0.77	3.50×10^{-3}	1.11	7.75×10^{-2}	0.99	9.26×10^{-1}	NA	NA	4.47×10^{-2}	0.92 [0.85-1.00]	1.35×10^{-4}	*PIGK*	intron
2	rs72811720	56147089	C	T	2.01	5.47×10^{-4}	2.33	2.60×10^{-2}	1.67	6.96×10^{-2}	1.12	5.11×10^{-1}	1.85	1.44×10^{-1}	1.13	7.32×10^{-1}	7.43×10^{-5}	1.52 [1.24-1.88]	2.19×10^{-1}	*EFEMP1*	intron
2	rs752816	56258606	C	G	1.38	4.65×10^{-3}	1.31	9.08×10^{-2}	1.44	1.76×10^{-3}	0.98	7.80×10^{-1}	0.97	8.28×10^{-1}	1.03	8.38×10^{-1}	6.03×10^{-3}	1.14 [1.04-1.25]	2.06×10^{-2}	*LOC105374690 /MIR217HG*	intron/ intron
2	rs66974421	130401804	G	A	1.28	1.57×10^{-3}	1.30	3.78×10^{-2}	1.18	3.47×10^{-2}	0.97	5.20×10^{-1}	0.99	8.99×10^{-1}	NA	NA	1.83×10^{-2}	1.08 [1.01-1.16]	8.72×10^{-3}	*LOC105373614*	5' flanking
2	rs16861684	174306514	G	A	1.29	5.66×10^{-4}	1.31	2.96×10^{-2}	1.12	1.42×10^{-1}	0.94	1.89×10^{-1}	0.91	3.69×10^{-1}	1.04	7.26×10^{-1}	1.01×10^{-1}	1.05 [0.99-1.12]	2.22×10^{-3}	*LOC105373744*	intron
2	rs75295922	207814273	C	A	1.40	2.40×10^{-3}	1.36	9.35×10^{-2}	1.47	5.88×10^{-5}	1.05	5.24×10^{-1}	1.05	7.05×10^{-1}	0.82	1.75×10^{-1}	2.94×10^{-4}	1.18 [1.08-1.29]	3.61×10^{-3}	*CPO*	intron
3	rs936154	36487492	G	A	1.22	2.13×10^{-2}	1.68	6.33×10^{-4}	1.24	3.19×10^{-2}	1.05	3.63×10^{-1}	1.15	2.05×10^{-1}	1.39	2.40×10^{-2}	2.52×10^{-5}	1.17 [1.09-1.26]	6.39×10^{-2}	*STAC*	intron
4	rs219474	109313182	C	A	1.31	9.09×10^{-4}	1.26	1.08×10^{-1}	1.22	2.50×10^{-2}	1.09	1.26×10^{-1}	0.97	8.11×10^{-1}	0.94	6.09×10^{-1}	4.62×10^{-4}	1.13 [1.06-1.21]	1.14×10^{-1}	*LOC107986301*	3' flanking
4	rs2611259	166619952	A	G	0.80	7.62×10^{-3}	0.90	4.59×10^{-1}	0.72	3.64×10^{-5}	0.93	2.53×10^{-1}	0.93	4.71×10^{-1}	1.03	7.96×10^{-1}	6.35×10^{-5}	0.87 [0.81-0.93]	6.10×10^{-2}	*LINC01179*	intron
4	rs2720378	185568113	C	G	0.64	2.52×10^{-8}	0.83	1.51×10^{-1}	0.81	6.60×10^{-3}	0.85	1.66×10^{-3}	1.00	9.63×10^{-1}	1.03	7.79×10^{-1}	**1.56×10^{-8}**	0.83 [0.78-0.89]	2.89×10^{-3}	*CASP3*	intron
4	rs72693559	185856229	A	G	0.76	1.08×10^{-2}	0.60	1.15×10^{-2}	0.78	1.97×10^{-2}	1.01	9.24×10^{-1}	0.95	7.19×10^{-1}	1.00	9.96×10^{-1}	8.72×10^{-3}	0.89 [0.81-0.97]	5.45×10^{-2}	*MIR4455*	3' flanking
5	rs34920909	36792716	G	C	1.34	1.42×10^{-4}	1.28	5.53×10^{-2}	1.15	6.72×10^{-2}	0.98	6.98×10^{-1}	1.13	1.93×10^{-1}	1.08	4.76×10^{-1}	7.12×10^{-4}	1.12 [1.05-1.19]	3.08×10^{-2}	*LOC107986412*	5' flanking
5	rs918557	61379277	T	C	1.33	2.04×10^{-4}	1.22	1.04×10^{-1}	1.05	5.20×10^{-1}	1.04	4.98×10^{-1}	0.97	7.56×10^{-1}	0.96	7.42×10^{-1}	1.38×10^{-2}	1.08 [1.02-1.15]	4.53×10^{-2}	*LOC105378998*	intron
5	rs62391744	126165480	A	C	0.67	7.93×10^{-3}	0.65	5.31×10^{-2}	0.66	3.28×10^{-3}	1.01	8.86×10^{-1}	0.90	4.85×10^{-1}	1.06	7.73×10^{-1}	6.41×10^{-3}	0.85 [0.76-0.96]	3.78×10^{-2}	*LMNB1*	intron
6	rs407934	25504562	C	T	0.71	9.25×10^{-4}	0.77	6.13×10^{-2}	0.68	9.37×10^{-5}	0.88	5.22×10^{-2}	0.74	3.47×10^{-3}	1.17	2.24×10^{-1}	1.57×10^{-7}	0.81 [0.75-0.88]	9.03×10^{-3}	*CARMIL1*	intron
6	rs1873212	27869631	C	T	1.35	1.74×10^{-4}	1.43	1.72×10^{-2}	1.29	1.24×10^{-2}	1.20	1.76×10^{-3}	1.34	1.27×10^{-2}	1.17	2.75×10^{-1}	**2.01×10^{-10}**	1.27 [1.18-1.36]	7.28×10^{-1}	*TRX-CAT1-7*	3' flanking
6	rs1778477	28248594	A	T	0.79	2.80×10^{-2}	0.66	7.19×10^{-3}	0.72	2.93×10^{-3}	0.76	7.07×10^{-5}	0.83	9.45×10^{-2}	0.84	3.08×10^{-1}	**7.24×10^{-10}**	0.77 [0.70-0.83]	8.26×10^{-1}	*PGBD1*	5' flanking
6	rs72843667	29812727	C	T	1.23	4.47×10^{-3}	1.28	5.55×10^{-2}	1.15	4.97×10^{-2}	1.10	6.83×10^{-2}	1.20	6.66×10^{-2}	1.04	6.95×10^{-1}	1.21×10^{-5}	1.15 [1.08-1.22]	6.56×10^{-1}	*LOC105375010*	3' flanking
6	rs1264516	30411903	C	A	1.31	5.16×10^{-4}	1.38	7.97×10^{-3}	1.20	2.69×10^{-2}	1.21	2.83×10^{-4}	1.29	3.48×10^{-3}	1.11	3.49×10^{-1}	**3.89×10^{-11}**	1.24 [1.16-1.32]	7.48×10^{-1}	*LOC105375012*	3' flanking
6	rs2857602	31533378	G	A	0.73	8.92×10^{-6}	0.67	1.21×10^{-3}	0.86	5.92×10^{-2}	0.77	2.48×10^{-7}	0.81	2.69×10^{-2}	0.84	1.27×10^{-1}	**2.78×10^{-15}**	0.78 [0.73-0.83]	4.28×10^{-1}	*LTA*	intron
6	rs3129960	32300809	A	G	0.72	3.50×10^{-4}	0.84	3.67×10^{-1}	0.75	1.75×10^{-3}	0.66	7.08×10^{-8}	0.83	2.23×10^{-1}	0.83	1.71×10^{-1}	**6.67×10^{-13}**	0.73 [0.67-0.80]	5.84×10^{-1}	*C6orf10/ LOC101929163*	intron/ intron
6	rs9380293	32377284	C	T	1.40	1.30×10^{-5}	1.17	3.35×10^{-1}	1.01	9.48×10^{-1}	1.27	4.44×10^{-5}	1.09	4.97×10^{-1}	1.18	1.93×10^{-1}	4.97×10^{-8}	1.22 [1.14-1.31]	1.17×10^{-1}	*BTNL2*	5' flanking
6	rs984778	32400088	C	T	0.70	1.33×10^{-6}	1.13	3.65×10^{-1}	0.81	7.76×10^{-3}	0.86	3.73×10^{-3}	1.08	4.48×10^{-1}	0.90	3.61×10^{-1}	1.39×10^{-6}	0.85 [0.80-0.91]	3.56×10^{-3}	*HLA-DRA*	5' flanking
6	rs9270957	32573235	A	G	0.65	3.71×10^{-7}	0.91	5.50×10^{-1}	0.91	3.10×10^{-1}	0.95	4.12×10^{-1}	NA	NA	NA	NA	2.75×10^{-4}	0.86 [0.80-0.93]	2.44×10^{-3}	*HLA-DRB1*	5' flanking
6	rs7775228	32658079	T	C	1.29	5.39×10^{-4}	1.07	5.96×10^{-1}	1.35	1.98×10^{-4}	1.36	3.07×10^{-9}	1.05	6.48×10^{-1}	1.08	5.36×10^{-1}	**6.99×10^{-13}**	1.26 [1.19-1.35]	7.63×10^{-2}	*HLA-DQB1*	5' flanking
6	rs2071473	32782605	C	T	1.39	8.37×10^{-6}	1.32	2.26×10^{-2}	1.09	2.62×10^{-1}	1.29	1.22×10^{-6}	1.30	6.06×10^{-3}	1.15	2.25×10^{-1}	**6.68×10^{-13}**	1.26 [1.18-1.34]	2.28×10^{-1}	*HLA-DOB*	intron
6	rs9480311	156667058	C	A	1.39	4.29×10^{-4}	1.18	3.32×10^{-1}	1.25	1.83×10^{-2}	1.02	7.99×10^{-1}	1.05	7.09×10^{-1}	1.02	9.15×10^{-1}	1.61×10^{-3}	1.14 [1.05-1.24]	1.04×10^{-1}	*LOC101928923*	intron
7	rs75400473	52779924	T	C	1.28	3.48×10^{-3}	1.56	1.51×10^{-3}	1.18	8.02×10^{-2}	1.05	4.58×10^{-1}	NA	NA	NA	NA	2.22×10^{-4}	1.17 [1.08-1.27]	3.37×10^{-2}	*LOC101928257*	5' flanking
7	rs77282866	52823787	G	T	1.46	1.04×10^{-3}	1.90	3.40×10^{-4}	1.21	2.01×10^{-1}	0.98	7.86×10^{-1}	0.85	2.85×10^{-1}	0.80	2.70×10^{-1}	2.44×10^{-2}	1.13 [1.02-1.26]	3.52×10^{-4}	*LOC101928257*	5' flanking
7	rs41830	106261427	T	C	1.23	2.71×10^{-2}	1.44	1.77×10^{-2}	1.16	8.57×10^{-2}	0.94	3.98×10^{-1}	0.86	1.79×10^{-1}	1.11	4.05×10^{-1}	9.83×10^{-2}	1.07 [0.99-1.15]	1.53×10^{-2}	*CTB-30L5.1*	intron
7	rs1791001	134125056	G	C	0.79	1.69×10^{-2}	0.60	1.45×10^{-3}	0.84	5.70×10^{-2}	1.05	4.34×10^{-1}	1.03	8.18×10^{-1}	NA	NA	3.86×10^{-2}	0.92 [0.85-1.00]	3.31×10^{-3}	*AKR1B1*	3' flanking
8	rs2736340	11343973	C	T	1.71	1.34×10^{-9}	1.48	6.12×10^{-3}	1.56	1.98×10^{-7}	1.51	6.19×10^{-13}	1.48	3.82×10^{-4}	1.55	7.65×10^{-4}	6.62×10^{-3}	1.55 [1.44-1.66]	8.96×10^{-1}	*BLK*	5' flanking
10	rs4417171	28025034	C	G	1.31	4.31×10^{-4}	1.13	3.86×10^{-1}	1.22	8.85×10^{-3}	0.95	4.12×10^{-1}	1.26	3.95×10^{-2}	1.16	1.68×10^{-1}	4.75×10^{-4}	1.13 [1.05-1.20]	1.25×10^{-2}	*MKX*	intron
10	rs2251348	117952736	C	T	1.37	1.30×10^{-4}	1.14	3.98×10^{-1}	1.33	3.90×10^{-3}	1.02	6.92×10^{-1}	0.89	3.41×10^{-1}	1.14	3.07×10^{-1}	1.01×10^{-3}	1.13 [1.05-1.22]	1.07×10^{-2}	*GFRA1*	intron
11	rs113420414	11405402	C	T	1.47	1.51×10^{-4}	1.84	2.30×10^{-3}	1.14	2.56×10^{-1}	1.17	3.44×10^{-2}	NA	NA	NA	NA	3.09×10^{-6}	1.27 [1.15-1.40]	5.13×10^{-2}	*GALNT18*	intron
12	rs7963257	97916472	A	G	1.27	1.37×10^{-2}	1.77	3.59×10^{-4}	1.20	2.91×10^{-2}	1.10	1.43×10^{-1}	1.29	2.2×10^{-2}	1.14	2.63×10^{-1}	1.22×10^{-6}	1.20 [1.12-1.29]	1.11×10^{-1}	*RMST*	intron
13	rs12428318	29096824	C	T	0.71	3.86×10^{-6}	0.95	6.69×10^{-1}	0.87	6.58×10^{-2}	0.94	2.31×10^{-1}	0.97	7.39×10^{-1}	1.11	3.30×10^{-1}	7.03×10^{-4}	0.90 [0.84-0.96]	7.73×10^{-3}	*FLT1*	5' flanking
14	rs9322955	35975341	A	G	0.79	1.39×10^{-2}	0.87	3.52×10^{-1}	0.73	1.38×10^{-4}	1.19	1.74×10^{-2}	1.18	1.27×10^{-1}	1.22	1.10×10^{-1}	4.41×10^{-1}	0.97 [0.90-1.05]	7.94×10^{-6}	*LOC107984681*	3' flanking
14	rs10145910	52334931	C	T	0.78	6.45×10^{-3}	0.86	2.62×10^{-1}	0.77	1.81×10^{-3}	0.99	8.64×10^{-1}	1.01	9.04×10^{-1}	0.97	7.81×10^{-1}	3.81×10^{-3}	0.90 [0.84-0.97]	7.75×10^{-2}	*GNG2*	intron
14	rs4774175	107152027	G	A	1.22	4.86×10^{-3}	1.40	7.57×10^{-3}	1.16	4.20×10^{-2}	1.22	1.69×10^{-4}	1.20	5.95×10^{-2}	1.06	6.34×10^{-1}	**6.01×10^{-9}**	1.20 [1.13-1.28]	6.90×10^{-1}	*IGHV1-69*	3' flanking
15	rs11631322	70479558	C	T	1.26	4.21×10^{-1}	2.78	4.98×10^{-4}	1.71	1.41×10^{-3}	1.16	4.97×10^{-1}	0.75	3.00×10^{-1}	1.06	8.39×10^{-1}	9.03×10^{-4}	1.39 [1.14-1.68]	1.87×10^{-2}	*LOC107984734*	5' flanking
16	rs13330932	85974507	C	T	1.26	2.32×10^{-3}	1.12	4.18×10^{-1}	1.48	9.60×10^{-7}	0.96	4.67×10^{-1}	1.05	6.34×10^{-1}	0.95	7.04×10^{-1}	1.03×10^{-3}	1.12 [1.05-1.20]	2.21×10^{-4}	*LOC107984811*	5' flanking
17	rs55809698	49504291	G	A	1.19	1.82×10^{-2}	1.09	4.94×10^{-1}	1.34	4.05×10^{-5}	1.04	3.99×10^{-1}	NA	NA	0.97	8.13×10^{-1}	3.08×10^{-4}	1.13 [1.06-1.20]	3.32×10^{-2}	*LOC105371828*	5' flanking
18	rs4799377	32844749	T	G	1.20	1.92×10^{-2}	1.48	2.48×10^{-3}	1.18	2.20×10^{-2}	0.89	3.55×10^{-2}	1.05	5.87×10^{-1}	0.99	8.94×10^{-1}	1.08×10^{-1}	1.05 [0.99-1.12]	6.10×10^{-4}	*ZSCAN30*	intron
19	rs11670224	17238170	C	T	0.74	5.31×10^{-4}	0.72	2.41×10^{-2}	0.87	1.15×10^{-1}	1.01	8.53×10^{-1}	1.00	9.86×10^{-1}	NA	NA	4.77×10^{-3}	0.89 [0.83-0.97]	1.98×10^{-2}	*MYO9B*	intron
19	rs28493229	41224204	G	C	1.50	3.45×10^{-6}	0.98	9.13×10^{-1}	1.97	1.91×10^{-6}	1.38	1.26×10^{-6}	1.25	1.35×10^{-1}	1.24	2.73×10^{-1}	1.15×10^{-4}	1.41 [1.29-1.53]	5.35×10^{-2}	*ITPKC*	intron
20	rs6111093	16382725	T	A	0.79	2.73×10^{-3}	0.76	1.87×10^{-2}	0.86	3.31×10^{-2}	1.02	7.73×10^{-1}	1.07	4.87×10^{-1}	0.87	2.09×10^{-1}	6.49×10^{-3}	0.92 [0.86-0.98]	1.79×10^{-2}	*KIF16B*	intron
20	rs1883832	44746982	T	C	1.34	1.41×10^{-4}	1.07	6.09×10^{-1}	1.41	4.85×10^{-6}	1.18	2.12×10^{-3}	1.32	5.11×10^{-3}	1.42	2.26×10^{-3}	**1.45×10^{-13}**	1.28 [1.20-1.36]	2.12×10^{-1}	*CD40*	5' untranslated region

For all single nucleotide variants (SNVs), association in the allelic model was evaluated and odds ratios were calculated for the effects of the alternative alleles.

[a] Location of the SNVs are derived from NCBI human genome reference sequence Build 37.3.

[b] Combined odds ratios and P values were calculated using fixed-effects meta-analytic model. *P* values < 5.0×10^{-8} are bold faced.

GWAS, genome-wide association study; Ref, Reference allele; Alt, Alternative allele;OR, Odds ratio; CI, Confidence interval; QE P, P values for QE statistics in tests for residual heterogeneity

Supplementary Table 8. Association data of rs2875151 G/A in three Asian GWAS for KD susceptibility.

Population	**cases/controls**	**RAF in cases**	**RAF in controls**	**OR**	**95% CI**	***P***
Japan	428/3379	0.82	0.76	1.47	1.23-1.77	3.15×10^{-5}
Korea	186/600	0.76	0.73	1.16	0.88-1.53	0.29
Taiwan	622/1107	0.70	0.71	0.95	0.81-1.10	0.47

RAF and odds ratios were calculated on an assumption that the G allele was the risk allele.

RAF, risk allele frequency; OR, odds ratio; CI, confidence interval

Supplementary Table 9. Evaluation of the 7 newly identified significant SNVs in 6p21 region by linkage disequilibrium and logistic regression analyses with rs2857151

				Association statistics[a] OR (95% CI) $P_{logistic}$		
				SNV of interest		rs2857151
SNVs	Position	r^2 with rs2857151	Distance from rs2857151	Single-SNV	Conditional[b]	Conditional[c]
rs1873212	27869631	0.022	4893883	1.20 (1.07-1.34) 1.79×10^{-3}	1.14 (1.02-1.28) 0.0224	1.41 (1.25 - 1.59) 3.17×10^{-8}
rs1778477	28248594	0.05	4514920	1.32 (1.15-1.51) 7.45×10^{-5}	1.24 (1.08-1.43) 0.00229	1.40 (1.24 - 1.58) 5.06×10^{-8}
rs1264516	30411903	0.034	2351611	1.21 (1.09 - 1.34) 2.89×10^{-4}	1.16 (1.04-1.29) 0.00648	1.40 (1.24 - 1.59) 4.42×10^{-8}
rs2857602	31533378	0.083	1230136	1.30 (1.18 - 1.44) 2.69×10^{-7}	1.22 (1.10-1.35) 2.18×10^{-4}	1.36 (1.20 - 1.53) 1.78×10^{-6}
rs3129960	32300809	0.029	462705	1.51 (1.30-1.75) 8.53×10^{-8}	1.42 (1.22-1.66) 4.80×10^{-6}	1.40 (1.24 - 1.58) 7.08×10^{-8}
rs7775228	32658079	0.125	105435	1.36 (1.23-1.51) 3.59×10^{-9}	1.25 (1.12-1.40) 5.41×10^{-5}	1.33 (1.17-1.51) 1.57×10^{-5}
rs2857151	32763514	NA	0	1.45 (1.28-1.63) 1.35×10^{-9}	NA	NA
rs2071473	32782605	0.36	19091	1.29 (1.16-1.42) 1.30×10^{-6}	1.10 (0.97-1.25) 0.12	1.36 (1.18-1.57) 3.29×10^{-5}

KD, Kawasaki disease; SNV, single nucleotide variant; OR, odds ratio; CI, confidence interval.

[a] Association of the SNVs with KD was evaluted in Japanese KD cases (n=1418) and controls (n=1700) prepared as a follow-up sample panel.

[b] Association statistics for the SNVs in logistic regression analyses conditioned on rs2857151.

[c] Association statistics for rs2857151 in logistic regression analyses conditioned on the other SNV.

Supplementary Table 10. Association of rs6423677 and KD in the Korean and Taiwanese subjects.

Population	case-control sets	Data type	KD		Control		OR (95% CI)	P_{allele}
			n	RAF[a]	n	RAF*		
Korea	Replication	genotyped	568	0.603	556	0.577	1.11 (0.94 - 1.32)	0.22
Taiwan	GWAS	genotyped	91	0.545	188	0.500	1.21 (0.84 - 1.74)	0.30
Taiwan	Replication	genotyped	261	0.536	550	0.543	0.97 (0.79 - 1.20)	0.81

KD, Kawasaki disease; RAF, risk allele frequency; OR, odds ratio; CI, confidence interval

[a] C allele of rs6423677 was regarded as the risk allele.

Supplementary Table 11. Characteristics of the KD patients in the immunoglobulin heavy chain repertoire analyses.

Patient	Sex	Age at KD onset	Year and month at KD onset	Number of major symptoms seen in the patients	Response to the initial IVIG treatment	Coronary artery outcome	Genotype at rs6423677	Ethnicity	Illness days when blood samples were obtained			
									Acute phase before receiving IVIG	48 hours after the patients became afebrile	The first visit to the pediatric clinic after discharge	The second visit to the pediatric clinic after discharge
1	M	0y11m	May. 2016	4	Responded	none	CC	Mixed[a]	6	8	20	98
2	F	4y6m	May. 2016	6	Responded	none	AC	Japanese	3	5	17	94
3	M	4y0m	May. 2016	5	Responded	none	CC	Japanese	5	10	17	94
4	F	1y11m	June. 2016	5	Responded	none	AC	Japanese	5	10	17	108
5	M	8y11m	June. 2016	5	Not responded	none	AC	Japanese	8	18	50	113
6	M	2y8m	August. 2018	5	Responded	none	AC	Japanese	6	10	18	96
7	M	4y7m	July. 2018	5	Responded	none	AC	Filipino	5	11	22	92
8	F	4y2m	July. 2018	5	Responded	none	AA	Japanese	6	11	28	109
9	M	1y3m	July. 2018	5	Responded	none	CC	Japanese	3	8	19	89

[a] Japanese and Thai.

KD, Kawasaki disease; IVIG, intravenous immunoglobulin

All patients are residents of Chiba prefecture.

Supplementary Table 12. Verification of previously reported frequent CDR3 clonotypes of IgM heavy chains in the acute phase KD patients in Taiwan.

	Taiwan				Japan	
CDR3 clonotypes[a]	**KD patients (n=30)**		**Febrile controls (n=10)**		**KD patients (n=9)**	
	n	**%**	**n**	**%**	**n**	**%**
CARDYYYGMDVW	9	30.0	1	10.0	2	22.2
CARSDWFDPW	6	20.0	0	0.0	1	11.1
CARHDWFDPW	5	16.7	2	20.0	2	22.2
CARAGGYYYGMDVW	4	13.3	0	0.0	1	11.1
CARAGNYYYGMDVW	4	13.3	0	0.0	1	11.1
CARVDDYW	4	13.3	0	0.0	1	11.1
CAKSDWFDPW	4	13.3	0	0.0	0	0.0
CARDRSGWYYFDYW	4	13.3	2	20.0	0	0.0
CARDYGGNSGWFDPW	4	13.3	0	0.0	3	33.3
CARGVAAGVDYW	4	13.3	0	0.0	0	0.0
CARIGYSSSSFDYW	3	10.0	0	0.0	0	0.0
CARDSSGWYYFDYW	3	10.0	2	20.0	0	0.0
CAKDSSSWYYFDYW	3	10.0	1	10.0	0	0.0
CARDGYW	3	10.0	0	0.0	1	11.1
CARAGDYYYGMDVW	3	10.0	0	0.0	0	0.0
CARGYYYYMDVW	3	10.0	0	0.0	0	0.0
CARDGSSGWHFDYW	3	10.0	0	0.0	0	0.0
CARDVSGSLDYW	3	10.0	0	0.0	1	11.1
CARDRGDFDYW	3	10.0	0	0.0	0	0.0
CARGFDYW	3	10.0	0	0.0	1	11.1
CARAGSYRFDYW	3	10.0	2	20.0	0	0.0
CARDYYYYMDVW	3	10.0	0	0.0	1	11.1
CARGLYYFDYW	3	10.0	0	0.0	0	0.0
CARAGSFRFDYW	3	10.0	1	10.0	2	22.2
CARDGYNWNDFDYW	3	10.0	0	0.0	0	0.0
CGKDISPGGMDVW	3	10.0	0	0.0	0	0.0
CVRGGYWRFDYW	3	10.0	1	10.0	0	0.0
CTTDPRHW	3	10.0	0	0.0	0	0.0
CTTDPRYW	3	10.0	0	0.0	1	11.1
CARAGYYRFDYW	3	10.0	1	10.0	1	11.1
CARGRDYW	3	10.0	0	0.0	0	0.0
CARLPTGYPNWFDPW	3	10.0	0	0.0	0	0.0

[a] Thirty-two CDR3 clonotypes of IgM heavy chain transcript that had frequencies of 0.01% or higher among more than 10% of IVIG responsive KD patients in Taiwan when they had not received the treatment (reference #16) are shown.

Those with frequencies of 0.01% or higher in one or more Japanese KD patients in this study were boldfaced.

CDR3, complementarity determining region; KD, Kawasaki disease; IVIG, intravenous immunoglobulin

Supplementary Table 13. *IGHV*, *IGHD* and *IGHJ* genes involved in CDR3 clonotypes of IgM heavy chains commonly increased in the acute phase KD patients in Taiwan and Japan.

Patients	Genotype at rs6423677	*IGHV* gene	*IGHD* gene	*IGHJ* gene	CDR3[a]	Proportion[b]
1	CC	*V3-74*01*	.	*J5*02*	CARSDWFDPW	0.00036
		*V3-13*01*	*D3-22*01*	*J6*02*	CARAGGYYYGMDVW	0.00028
		*V3-13*01*	*D1-7*01*	*J6*02*	CARAGNYYYGMDVW	0.00028
		*V3-13*01*	*D6-13*01*	*J6*02*	CARAGNYYYGMDVW	0.00022
		*V3-7*01*	*D6-25*01*	*J4*02*	CARDGYW	0.00026
		*V3-7*01*	*D5-24*01*	*J4*02*	CARDGYW	0.00017
		*V3-74*01*	*D1-26*01*	*J4*02*	CARAGSFRFDYW	0.00015
		*V3-74*01*	*D3-10*01*	*J4*02*	CARAGYYRFDYW	0.00013
2	AC	*V3-7*01*	*D1-26*01*	*J4*02*	CARDVSGSLDYW	0.00015
		*V3-7*03*	*D1-26*01*	*J4*02*	CARDVSGSLDYW	0.00012
3	CC	*V6-1*01*	.	*J6*02*	CARDYYYGMDVW	0.00035
		*V4-4*02*	.	*J4*02*	CARVDDYW	0.00033
		*V4-4*02*	*D3-9*01*	*J4*02*	CARVDDYW	0.000051
		*V4-4*02*	*D5-5*01*	*J4*02*	CARVDDYW	0.000019
		*V4-34*01*	*D5-5*01*	*J4*02*	CARVDDYW	0.000012
		*V3-74*01*	*D1-26*01*	*J4*02*	CARAGSFRFDYW	0.00023
5	AC	*V1-8*01*	*D4-23*01*	*J5*02*	CARDYGGNSGWFDPW	0.000212
6	AC	*V1-8*01*	*D4-23*01*	*J5*02*	CARDYGGNSGWFDPW	0.00012
8	AA	*V3-53*01*	.	*J5*02*	CARHDWFDPW	0.00012
		*V1-8*01*	*D4-23*01*	*J5*02*	CARDYGGNSGWFDPW	0.00013
		*V3-48*02*	.	*J4*02*	CARGFDYW	0.00011
		*V3-21*01*	.	*J4*02*	CARGFDYW	0.000012
		*V3-33*01*	.	*J4*02*	CARGFDYW	0.000012
		*V3-15*01*	*D1-14*01*	*J4*02*	CTTDPRYW	0.00080
		*V3-15*01*	*D3-16*02*	*J4*02*	CTTDPRYW	0.00013
		*V3-15*01*	.	*J4*02*	CTTDPRYW	0.000024
		*V3-23*01*	*D1-14*01*	*J4*02*	CTTDPRYW	0.000012
9	CC	*V6-1*01*	.	*J6*02*	CARDYYYGMDVW	0.00058
		V3-66*04	.	*J5*02*	CARHDWFDPW	0.00020
		*V6-1*01*	.	*J6*03*	CARDYYYYMDVW	0.00019

[a] CDR3 clonotypes of IgM heavy chain transcript demosntrated as commonly increased ones in Table S7.

[b] *IGHV-IGHD-IGHD* combinations with proportions larger than 0.001% were shown.

CDR3, complementarity determining region; KD, Kawasaki disease